

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 19.3333 Seconds  
(without alignments)  
79.628 Million cell updates/sec

Title: US-10-001-938-19  
Perfect score: 84  
Sequence: 1 EAVEVLSDKHKREIYD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

No matches found

Search completed: October 21, 2005, 15:36:11  
Job time : 19.3333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 91.6667 Seconds  
(without alignments)  
89.381 Million cell updates/sec

Title: US-10-001-938-19  
Perfect score: 84  
Sequence: 1 EAYEVLSDKHKREIYD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
-----					

No matches found

Search completed: October 21, 2005, 15:35:11  
Job time : 91.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 25.6667 Seconds  
(without alignments)  
46.534 Million cell updates/sec

Title: US-10-001-938-19  
Perfect score: 84  
Sequence: 1 EAYEVLSDKHKREIYD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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No matches found

Search completed: October 21, 2005, 15:15:49  
Job time : 25.6667 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 15:30:41 ; Search time 94 Seconds  
(without alignments)  
71.062 Million cell updates

Title: US-10-001-938-19  
Perfect score: 84  
Sequence: 1 EAYEVLSDPKHKREIYD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1

Minimum	DB	seq	length:	16
Maximum	DB	seq	length:	16

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Post-processing: Minimum Match 100%
                  Maximum Match 100%
                  Listing first 45 s
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Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pcp.*
17:	/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pcp.*
18:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
19:	/cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*
20:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp.*
21:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	84	100.0	16	14	US-10-001-938-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-10-001-938-19  
; Sequence 19, Application US/10001938  
; Publication No. US20030031679A  
; GENERAL INFORMATION:

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:22 ; Search time 100.667 Seconds  
(without alignments)  
61.472 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	5 AAU98852	AAU98852 E.Coli DN
2	86	100.0	16	6 ABR55126	ABR55126 E. coli d

ALIGNMENTS

RESULT 1

AAU98852

ID AAU98852 standard; peptide; 16 AA.

XX

XX

AC AAU98852;

XX

XX

DT 22-AUG-2002 (first entry)

XX

DE E.Coli DNAJ 61 immunogenic peptide.

XX

XX

KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;

KW cytosolic; antiinflammatory; antibacterial; antiarthritic;

KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;

KW infectious disease; inflammatory bowel disease; cancer;

XX mucosal tolerisation; DNA vaccination; anergy induction.

XX Escherichia coli.

OS

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PN WO200236611-A2.

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PD

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PF 10-MAY-2002.

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XX 25-SEP-2002; 2002WO-US030578.  
PF  
XX  
XX 25-SEP-2001; 2001US-0325499P.  
PR  
XX 11-DEC-2001; 2001US-0339284P.  
PR  
XX  
XX PA (REGC ) UNIV CALIFORNIA.  
XX  
XX Alhani S, Martins A;  
PI  
XX WPI; 2003-430097/40.  
DR  
XX  
XX Modulating an immune response in a subject having an immune-related  
PT disorder, e.g. arthritis by administering an antigen-specific epitope and  
PT a cytokine or an agent that effects cytokine activity or expression.  
XX  
XX Disclosure; Page 9; 41pp; English.  
PS  
XX  
CC The invention relates to a novel method for modulating an immune response  
CC in a subject having an immune-related disorder. The method comprises: (a)  
CC administering an antigen-specific epitope, where administration provides  
CC epitope-specific T cell immune modulation; and (b) administering a  
CC cytokine, an agent that effects cytokine activity or expression, or an  
CC anticytokine therapy. The method of the invention has antiarthritic,  
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic, anti-  
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-  
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,  
CC dermatological, and antipsoriatic activity. The method is useful for  
CC modulating an immune response in a subject having an immune-related  
CC disorder. The present sequence is used in the exemplification of the  
CC invention  
XX  
XX SQ Sequence 16 AA;  
Query Match 100.0%; Score 86; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.7e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QKRAAYDQYGHAAFEQ 16  
| | | | | | | | | | | | | | | |  
Db 1 QKRAAYDQYGHAAFEQ 16

Search completed: October 21, 2005, 15:41:20  
Job time : 101.667 secs

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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 19.3333 Seconds  
(without alignments)  
79.628 Million cell updates/sec

Title: US-10-001-938-3  
Perfect score: 86  
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
-----				

No matches found

Search completed: October 21, 2005, 15:36:11  
Job time : 19.3333 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 91.6667 Seconds  
(without alignments)  
89.381 Million cell updates/sec

Title: US-10-001-938-3  
Perfect score: 86  
Sequence: 1 QKEAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
-----						

No matches found

Search completed: October 21, 2005, 15:35:10  
Job time : 99.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 25.6667 Seconds  
(without alignments)  
46.534 Million cell updates/sec

Title: US-10-001-938-3  
Perfect score: 86  
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: October 21, 2005, 15:15:49  
Job time : 25.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:30:41 ; Search time 94 Seconds  
(without alignments)  
71.062 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	16	14	US-10-001-938-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-10-001-938-3  
; Sequence 3, Application US/10001938  
; Publication No. US20030031679A1  
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: ALBANI, Salvatore  
; APPLICANT: CARSON, Dennis  
; APPLICANT: PRAKKEN, Berent  
; APPLICANT: MARTINI, Alberto  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US  
; FILE REFERENCE: UCSD1360-1  
; CURRENT APPLICATION NUMBER: US/10/001,938  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-001-938-3

Query Match 100.0%; Score 86; DB 14; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16  
| | | | | | | | | | | | | | | |  
Db 1 QKRAAYDQYGHAAFEQ 16

Search completed: October 21, 2005, 15:48:52  
Job time : 94 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:22 ; Search time 100.667 Seconds  
(without alignments)  
61.472 Million cell updates/sec

Title: US-10-001-938-19  
Perfect score: 84  
Sequence: 1 EAYEVLSDKHKREIYD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	16	2	AAW59453 Human H5J
2	84	100.0	16	5	Aau98868 Human H5J
3	84	100.0	16	6	ABR55150 Human 51(

ALIGNMENTS

RESULT 1  
AAW59453  
ID AAW59453 standard; peptide; 16 AA.  
XX  
AC AAW59453;  
XX  
DT 28-AUG-1998 (first entry)  
XX  
DE Human H5J-1a protein DnaJ domain antigenic peptide fragment.  
XX  
KW Tumour-associated antigen; h-Tid; polyclonal antibody; human; H5J-1a;  
KW DnaJ domain; detection; colonic; endometrial; adenocarcinoma; mammary;  
KW pulmonary; cervical; carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN DE19702065-C1.

XX PD 20-MAY-1998.  
XX PF 22-JAN-1997; 97DE-01002065.  
XX PR 22-JAN-1997; 97DE-01002065.  
XX PA (KURZ/) KURZIK-DUMKE U.  
XX PI Kurzik-Dumke U;  
XX DR WPI; 1998-262548/24.  
XX PT Polyclonal antibody for detection of tumour-associated antigen hTid -  
XX PF useful in assays for diagnosis of cancer.  
XX PS Claim 1; Col 5; 4pp; German.  
XX CC This peptide fragment is derived from the human H5J-1a protein DnaJ  
CC domain and is used to raise polyclonal antibodies for detection of the  
CC tumour-associated antigen hTid. The antibody is used in an ELISA assay  
CC for hTid in a sample of body fluid or tissue extract, especially for  
CC detecting pathologically altered hTid expression in cells. The detection  
CC method involves immobilising the sample on a solid support, contacting  
CC the sample with the antibody, adding an antibody that specifically binds  
CC to the first antibody and is labelled with an enzyme that catalyses the  
CC conversion of a colourless substrate to a coloured product, adding the  
CC colourless substrate, and measuring the coloured product. The assay  
CC provides a simple and unequivocal means of detecting the human hTid  
CC protein, expression of which is characteristic of colonic and endometrial  
CC adenocarcinoma and mammary, pulmonary and cervical carcinoma  
XX SQ Sequence 16 AA;

Query Match 100.0%; Score 84; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAYEVLSDKHKREIYD 16  
| | | | | | | | | | | | | | | |  
Db 1 EAYEVLSDKHKREIYD 16

RESULT 2  
AAU98868  
ID AAU98868 standard; peptide; 16 AA.  
XX  
AC AAU98868;  
XX  
DT 22-AUG-2002 (first entry)  
XX  
DE Human H5J1 immunogenic peptide #5.  
XX  
KW Immunogenic peptide; heat shock protein; HSP; DnaJ; immunomodulatory;  
KW cytosolic; antiinflammatory; antibacterial; antiarthritic; human;  
KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;  
KW infectious disease; inflammatory bowel disease; cancer; H5J1;  
KW mucosal tolerisation; DNA vaccination; anergy induction.  
XX  
OS Homo sapiens.  
XX  
PN WO200236611-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 31-OCT-2001; 2001WO-US045344.  
XX  
PR 01-NOV-2000; 2000US-0245181P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI (MART/) MARTINI A.  
XX  
PI Martini A, Albani S, Carson DA, Prakken BJ;

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XX DR WPI; 2002-489999/52.
XX PT
XX PT New immunomodulatory peptides from heat shock proteins, useful for
XX PT treating immunological disorder in subjects such as humans, e.g.
XX PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
XX PT bowel disease or cancer.
XX PS
XX PS Claim 12; Page 57; 84pp; English.
XX CC
XX CC This invention relates to the use of a peptide, which is an immunogenic
XX CC portion derived from a dnaA heat shock protein (hsp) in modulating an
XX CC immune response in a subject. The peptides of the invention may have
XX CC immunomodulatory, cytostatic, antiinflammatory, antibacterial or
XX CC antiarthritic properties and can stimulate expression of interleukins,
XX CC tumour necrosis factor and transforming growth factor beta. The
XX CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
XX CC reducing/inhibiting) an immune response in a subject having an
XX CC immunological disorder (e.g. autoimmune disease such as arthritis or
XX CC articular juvenile idiopathic arthritis), an infectious disease, an
XX CC inflammatory bowel disease or cancer. The immunogenic peptide of the
XX CC invention is also useful for modulating immunoeffector cell
XX CC responsiveness in a subject. The immunogenic peptide is particularly
XX CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
XX CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
XX CC general, the peptide is useful in methods involving mucosal tolerisation,
XX CC DNA vaccination, anergy induction or active immunisation. The present
XX CC sequence represents a human heat shock protein immunogenic peptide of the
XX CC invention
XX SQ Sequence 16 AA;
      Query Match      100.0%; Score 84; DB 5; Length 16;
      Best Local Similarity 100.0%; Pred. No. 9.2e-07;
      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYEVLSDKHKREIYD 16
Db 1 EAYEVLSDKHKREIYD 16

RESULT 3
ABR55150
ID ABR55150 standard; peptide; 16 AA.
XX AC
XX AC ABR55150;
XX DT
XX DT 03-JUL-2003 (first entry)
XX DE
XX DE Human 51(HSJ1) antigen-specific epitope peptide.
XX KW
XX KW Antigen-specific epitope; immune response; T cell; cytokine;
XX KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
XX KW cytosratic; antithyroid; anti-asthmatic; immunosuppressive;
XX KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
XX KW antiallergic; dermatological; antipsoriatic; human.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO2003026579-A2.
XX XX
XX XX 03-APR-2003.
XX PF
XX PF 25-SEP-2002; 2002WO-US030578.
XX PR
XX PR 25-SEP-2001; 2001US-0325499P.
XX PR 11-DEC-2001; 2001US-0339284P.
XX XX
XX XX (REGC ) UNIV CALIFORNIA.
XX FA
XX FA Albani S, Martins A;
XX PI
XX PI WPI; 2003-430097/40.
XX DR

XX PT
XX PT Modulating an immune response in a subject having an immune-related
XX PT disorder, e.g. arthritis by administering an antigen-specific epitope and
XX PT a cytokine or an agent that effects cytokine activity or expression.
XX PS
XX PS Disclosure; Page 9; 41pp; English.
XX CC
XX CC The invention relates to a novel method for modulating an immune response
XX CC in a subject having an immune-related disorder. The method comprises: (a)
XX CC administering an antigen-specific epitope, where administration provides
XX CC epitope-specific T cell immune modulation; and (b) administering a
XX CC cytokine, an agent that effects cytokine activity or expression, or an
XX CC anticytokine therapy. The method of the invention has antiarthritic,
XX CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic, anti-
XX CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
XX CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
XX CC dermatological, and antipsoriatic activity. The method is useful for
XX CC modulating an immune response in a subject having an immune-related
XX CC disorder. The present sequence is used in the exemplification of the
XX CC invention
XX SQ Sequence 16 AA;
      Query Match      100.0%; Score 84; DB 6; Length 16;
      Best Local Similarity 100.0%; Pred. No. 9.2e-07;
      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYEVLSDKHKREIYD 16
Db 1 EAYEVLSDKHKREIYD 16

Search completed: October 21, 2005, 15:41:21
Job time : 101.667 secs

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